

```

GCGCGCGGCCA ACACGCCGAA TCGCCAGCCG GCGCATCCCA ACCCAGCACC TCGCGCGGCC 300
GACCGGAACG CACCGCGCGC ACTGTCTATT GCGCGAAGC CACCGCAACC TGTCCGGATC 360
GACRACCCGG TTGGAGGATT CAGCTTCGGG CTGCTCTCTG GCTGGGTGGA GTCTGACGCC 420
GCCACTTTCG ACTACGGTTC AGCACTCTTC AGCAAAACCA CCGGGGACCC GCCATTTCCC 480
GGACAGCGGC CCGCGGTGGC CAATGACACC CGTATCTGCG TCGCGCGGCT AGACCAAAAG 540
CTTTACGCCA GCGCGAAGC CACCGACTCC AAGCGCGCGG CCGCGTTGGG CTGGGACATG 600
GCTGAGTTCT ATATGCCCTA CCGCGGCACC CGGATCAACC AGGAAACCGT CTGCTCTGAC 660
GCCAACCGCG TGTCTGGAAG CCGCTCTAT TACGAAGTCA AGTTGAGCHA TCGGAGTAG 720
CGGAACGCGC AGATCTGGAC GCGCGTAATC GCTCGCGCG CCGCGAAGCG ACCCGACGCC 780
GCGCGCGCTC AGCGCTGGT TGTGCTATGG CTGGGAGCG CCAACAACCC GGTGGACAAG 840
GCGCGCGCCA AGCGCTGGC CGAATCGATC CCGCTTTGG TCGCGCGCGC GCGCGCGCGC 900
GCACCGCTTC CTGCAGAGC CGCTCGCGCG CCGCGCGCGC CCGCGGAAGT CGCTCTACC 960
CGGACGACAC CGACACCGCA GCGGACCTTA CCGCGCTGA 999

```

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1           5           10           15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20           25           30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35           40           45

Gln Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50           55           60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65           70           75           80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85           90           95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro

```

100	105	110
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser 115 120 125		
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp 130 135 140		
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro 145 150 155 160		
Gly Glu Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg 165 170 175		
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala 180 185 190		
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro 195 200 205		
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val 210 215 220		
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys 225 230 235 240		
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn 245 250 255		
Ala Pro Asp Ala Gly Pro Pro Glu Arg Trp Phe Val Val Trp Leu Gly 260 265 270		
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu 275 280 285		
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro 290 295 300		
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr 305 310 315 320		
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala 325 330		

## (C) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Asn Asn Tyr Gly Gln Val

1	5	10	15
Val Ala Ala Leu			
	20		

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5					10						15

Glu Gly Arg

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1				5					10					15

## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val  
1                  5                  10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 13 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro  
1                  5                  10

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 17 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro  
1                  5                  10                  15

Ala

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 15 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly  
1                  5                  10                  15

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 30 amino acids  
  (B) TYPE: amino acid  
  (C) STRANDEDNESS:  
  (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
1           5           10           15

Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
      20           25           30

```

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

Gly Cys Gly Asp Arg Ser Gly Gly Asn Leu Asp Gln Ile Arg Leu Arg
1           5           10           15

Arg Asp Arg Ser Gly Gly Asn Leu
      20

```

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Gln Arg Lys
1           5           10           15

Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
      20           25           30

Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala
      35           40           45

Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
      50           55           60

Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
      65           70           75           80

Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
      85           90           95

Asn Lys Gly Ser Leu Val Gln Gly Gly Ile Gly Gly Thr Gln Ala Arg
      100           105           110

```

```

Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
 115                      120                      125

Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
 130                      135                      140

Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
 145                      150                      155                      160

Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
                      165                      170                      175

Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
 180                      185

```

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1           5           10           15

Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
          20           25           30

Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
 15           40           45

Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser
 50           55           60

Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
 65           70           75           80

Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
          85           90           95

Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
        100           105           110

Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
        115           120           125

Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
        130           135           140

Thr Gly Gly Pro
145

```

## (2) INFORMATION FOR SEQ ID NO:66:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1           5           10           15

Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
20           25           30

Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser
35           40           45

Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
50           55           60

Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
65           70           75           80

Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Gln
85           90           95

Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
100          105          110

Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
115          120          125

Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
130          135          140

Ser Ala Ala Thr Ser Ser Thr Pro Arg Gln Ala Pro Tyr Glu Leu Asn
145          150          155          160

Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
165          170          175

Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
180          185          190

Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
195          200          205

Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
210          215          220

Phe Pro Ile Val Ala Arg
225          230

```

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20           25           30

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35           40           45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50           55           60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65           70           75           80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85           90           95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100          105          110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115          120          125

Gly Pro Pro Ala
130

```

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1           5           10           15

Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro
20           25           30

Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35           40           45

```



```

Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
 50                      55                      60

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
 65                      70                      75                      80

Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
 85                      90                      95

Ser Glu Arg Lys
100

```

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
 1                      5                      10                      15

Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20                      25                      30

Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35                      40                      45

Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50                      55                      60

Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65                      70                      75                      80

Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85                      90                      95

Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100                     105                     110

Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115                     120                     125

Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130                     135                     140

His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145                     150                     155                     160

Asp Arg Arg

```

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1           5           10           15

Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20           25           30

Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35           40           45

Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Glu Val Pro
50           55           60

Arg Gly Arg Lys Glu Ala Val Ala Ala Ala Val Ala Ala Ser Leu Arg
65           70           75           80

Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
85           90           95

Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
100          105          110

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
115          120          125

Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
130          135          140

Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
145          150          155          160

Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
165          170          175

Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
180          185          190

His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
195          200          205

Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
210          215          220

Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
225          230          235          240

```

Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro  
 245 250 255  
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro  
 260 265 270  
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala  
 275 280 285  
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu  
 290 295 300  
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr  
 305 310 315 320  
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln  
 325 330 335  
 Val Ser Arg Gln Asn Pro Thr Gly  
 340

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala  
 1 5 10 15  
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu  
 20 25 30  
 Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile  
 35 40 45  
 Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu  
 50 55 60  
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu  
 65 70 75 80  
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser  
 85 90 95  
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Ala Glu  
 100 105 110  
 Asp Glu Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala  
 115 120 125

Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met  
 130 135 140  
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro  
 145 150 155 160  
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala  
 165 170 175  
 Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu  
 180 185 190  
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly  
 195 200 205  
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser  
 210 215 220  
 Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser  
 225 230 235 240  
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser  
 245 250 255  
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu  
 260 265 270  
 Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr  
 275 280 285  
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile  
 290 295 300  
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp  
 305 310 315 320  
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala  
 325 330 335  
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn  
 340 345 350  
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp  
 355 360 365  
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp  
 370 375 380  
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala  
 385 390 395 400  
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu  
 405 410 415

```

Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
      420                      425                      430

Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
      435                      440                      445

Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
      450                      455                      460

Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
      465                      470                      475                      480

Val Ala Pro Thr Gly
      485

```

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
1           5           10           15

Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
      20           25           30

Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
      35           40           45

Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
      50           55           60

Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
      65           70           75           80

Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
      85           90           95

Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
      100          105          110

Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
      115          120          125

Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
      130          135          140

Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
      145          150          155          160

```

```

Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
      165                      170                      175

Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
      180                      185                      190

Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
      195                      200                      205

Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
      210                      215                      220

Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
      225                      230                      235                      240

Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
      245                      250                      255

Ala Pro Pro Pro Gln Ser Pro Ala Gln Gly Gly
      260                      265

```

## (2) INFORMATION FOR SEQ ID NO:73:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1           5           10           15

Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
20          25          30

Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
35          40          45

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
50          55          60

Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
65          70          75          80

Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Gln
85          90          95

Gln

```

## (3) INFORMATION FOR SEQ ID NO:74:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gly	Ala	Ala	Val	Ser	Leu	Leu	Ala	Ala	Gly	Thr	Leu	Val	Leu	Thr	Ala	1	5	10	15
Cys	Gly	Gly	Gly	Thr	Asn	Ser	Ser	Ser	Ser	Gly	Ala	Gly	Gly	Thr	Ser	20	25	30	
Gly	Ser	Val	His	Cys	Gly	Gly	Lys	Lys	Glu	Leu	His	Ser	Ser	Gly	Ser	35	40	45	
Thr	Ala	Gln	Glu	Asn	Ala	Met	Glu	Gln	Phe	Val	Tyr	Ala	Tyr	Val	Arg	50	55	60	
Ser	Cys	Pro	Gly	Tyr	Thr	Leu	Asp	Tyr	Asn	Ala	Asn	Gly	Ser	Gly	Ala	65	70	75	80
Gly	Val	Thr	Gln	Phe	Leu	Asn	Asn	Glu	Thr	Asp	Phe	Ala	Gly	Ser	Asp	85	90	95	
Val	Pro	Leu	Asn	Pro	Ser	Thr	Gly	Gln	Pro	Asp	Arg	Ser	Ala	Glu	Arg	100	105	110	
Cys	Gly	Ser	Pro	Ala	Trp	Asp	Leu	Pro	Thr	Val	Phe	Gly	Pro	Ile	Ala	115	120	125	
Ile	Thr	Tyr	Asn	Ile	Lys	Gly	Val	Ser	Thr	Leu	Asn	Leu	Asp	Gly	Pro	130	135	140	
Thr	Thr	Ala	Lys	Ile	Phe	Asn	Gly	Thr	Ile	Thr	Val	Trp	Asn	Asp	Pro	145	150	155	160
Gln	Ile	Gln	Ala	Leu	Asn	Ser	Gly	Thr	Asp	Leu	Pro	Pro	Thr	Pro	Ile	165	170	175	
Ser	Val	Ile	Phe	Arg	Ser	Asp	Lys	Ser	Gly	Thr	Ser	Asp	Asn	Phe	Gln	180	185	190	
Lys	Tyr	Leu	Asp	Gly	Val	Ser	Asn	Gly	Ala	Trp	Gly	Lys	Gly	Ala	Ser	195	200	205	
Glu	Thr	Phe	Ser	Gly	Gly	Val	Gly	Val	Gly	Ala	Ser	Gly	Asn	Asn	Gly	210	215	220	
Thr	Ser	Ala	Leu	Leu	Gln	Thr	Thr	Asp	Gly	Ser	Ile	Thr	Tyr	Asn	Gln	225	230	235	240
Trp	Ser	Phe	Ala	Val	Gly	Lys	Gln	Leu	Asn	Met	Ala	Gln	Ile	Ile	Thr	245	250	255	

Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys  
 260 265 270  
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu  
 275 280 285  
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile  
 290 295 300  
 Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr  
 305 310 315 320  
 Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly  
 325 330 335  
 Gln Gln Gly Leu Asp Glu Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe  
 340 345 350  
 Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser  
 355 360

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp  
 1 5 10 15  
 Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val  
 20 25 30  
 Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro  
 35 40 45  
 Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser  
 50 55 60  
 Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg  
 65 70 75 80  
 Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro  
 85 90 95  
 Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg  
 100 105 110  
 Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp  
 115 120 125



Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val  
 130 135 140  
 Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg  
 145 150 155 160  
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly  
 165 170 175  
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala  
 180 185 190  
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val  
 195 200 205  
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg  
 210 215 220  
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro  
 225 230 235 240  
 Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg  
 245 250 255  
 Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His  
 260 265 270  
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr  
 275 280 285  
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg  
 290 295 300  
 Asn Arg Pro Arg Arg  
 305

## (3) INFORMATION FOR SEQ ID NO:76:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly  
 1 5 10 15  
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys  
 20 25 30  
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala  
 35 40 45

Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys  
 50 55 60  
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr  
 65 70 75 80  
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser  
 85 90 95  
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His  
 100 105 110  
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln  
 115 120 125  
 Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro  
 130 135 140  
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Gln Thr  
 145 150 155 160  
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln  
 165 170 175  
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro  
 180 185 190  
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met  
 195 200 205  
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr  
 210 215 220  
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val  
 225 230 235 240  
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala  
 245 250 255  
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val  
 260 265 270  
 Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Gln Thr  
 275 280 285  
 Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala  
 290 295 300  
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Ala Lys  
 305 310 315 320  
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp  
 325 330 335  
 Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp

340	345	350
Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser		
355	360	365
Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile		
370	375	380
Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser		
385	390	395
Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn		
405	410	415
Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn		
420	425	430
Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn		
435	440	445
Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly		
450	455	460
Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile		
465	470	475
Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly		
485	490	495
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu		
505	510	515
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val		
525	530	535
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu		
540	545	550
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr		
555	560	565
Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly		
570	575	
Lys Ala Glu Gln		
580		

## (2) INFORMATION FOR SEQ ID NO:77:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
1           5           10           15

Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
20           25           30

Asp Ala Glu Glu Glu Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
35           40           45

Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
50           55           60

Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu
65           70           75           80

Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala
85           90           95

Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg
100          105          110

Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
115          120          125

Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
130          135          140

Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
145          150          155          160

Gly Thr Gln Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
165          170          175

Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
180          185          190

Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
195          200          205

Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
210          215          220

Lys Trp Asn Glu Pro Val Asn Val Asp
225          230

```

## (2) INFORMATION FOR SEQ ID NO:78:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
1           5           10           15
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
20           25           30
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
15           40           45
Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
50           55           60
Pro Arg
65

```

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
1           5           10           15
Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
20           25           30
Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
35           40           45
Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
50           55           60
Ser Pro Pro Leu Pro
65

```

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
1           5           10           15

```

Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala  
 20 25 30  
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu  
 35 40 45  
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val  
 50 55 60  
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr  
 65 70 75 80  
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val  
 85 90 95  
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln  
 100 105 110  
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala  
 115 120 125  
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly  
 130 135 140  
 Gly Gly Val Ala Val Gly Gln Pro Val Val Ala Met Gly Asn Ser Gly  
 145 150 155 160  
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu  
 165 170 175  
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Gln Gln Thr  
 180 185 190  
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser  
 195 200 205  
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr  
 210 215 220  
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala  
 225 230 235 240  
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly  
 245 250 255  
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu  
 260 265 270  
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val  
 275 280 285  
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile  
 290 295 300  
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp

```

308              310              315              320
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
              325              330              335

Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
              340              345              350

Pro Pro Ala
              355

```

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
1              5              10              15

Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala
              20              25              30

Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
              35              40              45

Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
              50              55              60

Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
              65              70              75              80

Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
              85              90              95

Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val
              100              105              110

Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
              115              120              125

Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys
              130              135              140

Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
              145              150              155              160

Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
              165              170              175

His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln

```

180

185

190

Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val  
 1 5 10 15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln  
 20 25 30

His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val  
 35 40 45

Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu  
 50 55 60

Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe  
 65 70 75 80

Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu  
 85 90 95

Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala  
 100 105 110

Ala Thr Glu Glu Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val  
 115 120 125

Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp  
 130 135 140

Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn  
 145 150 155 160

Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg  
 165 170 175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Gln Asn Ala Arg Gly  
 180 185 190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile  
 195 200 205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe



210	215	220
Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp		
225	230	235 240
Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg		
	245	250 255
Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln		
	260	265 270
Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys		
	275	280 285

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr		
1	5	10 15
Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp		
	20	25 30
Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg		
	35	40 45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg		
	50	55 60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro		
	65	70 75 80
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp		
	85	90 95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu		
	100	105 110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Glu Ile Glu Glu Val		
	115	120 125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn		
	130	135 140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro		
	145	150 155 160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu		

165

170

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Arg Ala Asp Gln Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
1           5           10           15

Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly
          20           25           30

Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
          35           40           45

Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
          50           55           60

Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
          65           70           75           80

Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Gln Gly Gly Ile
          85           90           95

Gly Gly Xaa Gln Gly Xaa Xaa Arg Arg Xaa Gln
          100          105

```

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
1           5           10           15

Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
          20           25           30

Arg Arg Ala Leu Gln Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly
          35           40           45

Val Lys Gln Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
          50           55           60

Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr

```

65		70		75		80
Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Glu						
	85			90		95
Glu Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr						
	100		105		110	
Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg						
	115		120		125	

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val									
1		5			10				15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala									
	20			25				30	
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu									
	35			40				45	
Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala									
	50			55			60		
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp									
65		70			75			80	
Gly Val Gln Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu									
	85			90				95	
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa									
	100			105				110	
Arg Ser Ser Xaa Gly									
	115								

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
1      5      10      15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
20      25      30
Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
35      40      45
Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
50      55      60
His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
65      70      75      80
Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
85      90      95
Pro Ala Ala Gly Gly Gly Ala
100
```

## (2) INFORMATION FOR SEQ ID NO: 88:

## (4) sequence characteristics.

- (C) LANGUAGE: English  
(C) DATE: 1978  
(C) SUBJECT: ~~Psychology~~  
(C) TOPIC: ~~Psychology~~

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11.

[illegible]

## (2) INFORMATION FOR SEQ ID NO: 30:

## (1) SEQUENCE CHARACTERISTICS:

- (3) 日期: 2010 年 10 月 10 日

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Thr Asp Ala Ala Thr Leu Ala Gln Gln Ala Gly Asn Phe Glu Arg Ile
1          5          10          15

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
20          25          30

Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
35          40          45

Ala Val Val Arg Phe Gln Gln Ala Ala Asn Lys Gln Lys Gln Glu Leu
50          55          60

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65          70          75          80

Ala Asp Gln Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
85          90          95

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1          5          10          15

Arg Ala Asn Gln Val Gln Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20          25          30

Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
35          40          45

Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
50          55          60

Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
65          70          75          80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85          90          95

Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100          105          110

Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115          120          125

```

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp  
 130 135 140

Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr  
 145 150 155 160

Leu Thr Leu Gln Gly Asp  
 155

## (2) INFORMATION FOR SEQ ID NO:91:

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Arg Ala Glu Arg Met  
 1 5

## (2) INFORMATION FOR SEQ ID NO:92:

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala  
 1 5 10 15

Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr  
 20 25 30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu  
 35 40 45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn  
 50 55 60

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe  
 65 70 75 80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe  
 85 90 95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala  
 100 105 110

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met

115	120	125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly		
130	135	140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro		
145	150	155
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met		
165	170	175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met		
180	185	190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala		
195	200	205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly		
210	215	220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala		
225	230	235
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly		
245	250	255
Arg Arg Asn Gly Gly Pro Ala		
260		

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala		
1	5	10
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly		
20	25	30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly		
35	40	45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr		
50	55	60
Gln Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro		
65	70	75
Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val		
80		

85	90	95
Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu 100	105	110
Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr 115	120	125
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln 130	135	140
Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr 145	150	155
Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg 165	170	175
Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly 180	185	190
Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln 195	200	205
Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser 210	215	220
Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala 225	230	235
Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser 245	250	255
Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Val Ser 260	265	270
Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn 275	280	285
Pro Ser Gly Gly Gln Gln Ser Ser Ser Pro Gly Gly Ala Pro Val 290	295	300

## (2) INFORMATION FOR SEQ ID NO:94:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAAGATGG TGAATCGAT CCCCACAGGT CTAACCCCGG CGCTTCGAT CCGCCCGCGT	60
CGCGCGCGTG TGAATTCGAT CATGGCTGGC GCGCCCGCTC TATACCGAT GCAGCCCGTC	120



```

GTCTTCGGCG CGCCACTGCC GTTGGACCCG GCATCCGCCC CTGACCTCCC GACCGCCGCC 180
CAGTTGACCA GCTCTCTCAA CAGCCTCCGC GATCCCAACG TGTCTTTTGC GAACAAGGCC 240
AGTCTGGTCS AGGGCCGCAT CCGGGGCACC GAGCCGCCCA TCGCCGACCA CAAGCTGAAG 300
AAGGCCGCCG AGCACGGGGA TCTCCGGCTG TCGTTCAGCG TGACGAACAT CCAGCCGGCG 360
GCCGCCGGTT CCGCCACCGC CGACGTTTCC GTCTCGGGTC CGAAGCTCTC GTCCCGGCTC 420
ACGCAGAACS TCACGTTCTT GAATCAAGGC GCTCGATGTC TGTCAAGCCG ATCGGCGATG 480
GAGTTGCTTC AGGCCGCAAG GAACTGA 507

```

## (2) INFORMATION FOR SEQ ID NO:95:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala 1
1 5 10 15
Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro 20
20 25 30
Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu 35
35 40 45
Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser 50
50 55 60
Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly 65
65 70 75 80
Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp 85
85 90 95
His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe 100
100 105 110
Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp 115
115 120 125
Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val 130
130 135 140
Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met 145
145 150 155 160

```

Glu Leu Leu Glu Ala Ala Gly Asn  
165

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

CGTGGCAATG TCGTTGACCG TCGGGGCGCG GGTGGCCTCC GCAGATCCCG TGGACCGCGT      60
CATTAAACCC ACCTGCAATT ACCGGCAGGT AGTAGCTGCG CTCACCGCGA CGGATCCCGG      120
GGCTGCCGCA CAGTTCAACG COTCACCGGT GGGCCAGTCC TATTTCGCA ATTTCCTCCG      180
CGCACCGCCA COTCAGCGCG CTGCCATGCC CGCCCAATTG CAAGCTGTTC CGGGGCGCGC      240
ACAGTACATC GGCCTTGTTC AGTGGGTTC CGGCTCCTGC AACCACTATT AAGGCCATGC      300
GGGCGGCATC CGGCGACCG GCATGCTGCC CGGGCTAGG CCAGATTGCC CGGCTCCTCA      360
ACGGGCGGCA TCGGGCGACC CGGCATGCTC GCGGGGGCTA GGGCAGATTG CCGGCTCCTT      420
CAACGGGCGG CATCTGCTGC CGAATTCCTG CAGCGCGCGG GATCCACTAG TTCTAGAGCG      480
GCGGCGCACTC CGGTGGAGCT
                                                                                      535

```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1           5           10           15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20           25           30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35           40           45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50           55           60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65           70           75           80

```

Gln Tyr Ile Gly Leu Val Gln Ser Val Ala Gly Ser Cys Asn Asn Tyr  
 85 90 95

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGGUC AATCCAGGGA 60  
 AATGTCAGCT CATTTCATTC GTCCTTGAC GAGGCGAAGC AGTCCCTGAC CAGCTCCCA 120  
 GCGGCGTGGG CCGGTAGCGG TTGGGAAGCG TACC 154

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser  
 1 5 10 15  
 Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly  
 20 25 30  
 Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser  
 35 40 45  
 Glu Ala Tyr  
 50

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGTCCGCGA CTTCAGGTC ACTATGAAAG TCGGCTCCG CTCAGAGAT TCGTGAACCT 60  
 TCAAGCGCGG CCGATAACTG AGGTGCATCA TTAAGCGACT TTCCCGAAC ATCGTGACCG 120

GCTCGAAACC	CGGCACAGCC	GACGGTGGCT	CCGNCGAGGC	GCTGNETCCA	AAATCCCTGA	180
GACAAATTCN	CGGGGCGGCC	TACAAGGAAG	TGGTGTCTGA	ATTGNCNGNG	TATCTGCTCG	240
ACCTGTGTGG	TCTGNAGCCG	GACGAAGCCG	TGCTCGACGT	CG		282

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3058 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATCGTACCC	GTGCGAGTGC	TGGGGCCGTT	TGAGGATGGA	GTGCACGTGT	CTTTCGTGAT	60
GGCATACCCA	GAGATGTTGG	CGGGCGCGGC	TGACACCTTG	CAGAGCATCG	GTGCTACCAC	120
TGTGGCTAGC	AATGCCGCTG	CGGCGGCCCC	GACGACTGGG	GTGGTGCCCC	CGGCTGCCGA	180
TGAGGTGTGG	GCGCTGACTG	CGGCGCACTT	CGCCGCACAT	GCGGCGATGT	ATCAGTCCGT	240
GAGCGGTGGG	GCTGCTGCGA	TTGATGACCA	GTTGCTGGCC	ACCTTTGCCA	GCAGCGCCAG	300
CTCGTATGCG	GCCACTGAAG	TGCGCAATGC	GGCGCGCGCC	AGCTAAGCCA	GGAACAGTCC	360
GCACGAGAAA	CGACGAGAAA	TAGGACACCG	TAATGTGTGA	TTTCGGGGCG	TTACCACCGG	420
AGATCAACTG	CGCGAGGATG	TACGCGCGCC	CGGGTTGCGC	CTCGCTGGTG	GCGCGGGCTC	480
AGATGTGGGA	CAGCGTGCGG	AGTGACCTGT	TTTCGGGGCG	CTCGGCTTTT	CACTCGGTGG	540
TCTGGGGTCT	GACGCTGGGG	TGTTGATAG	GTTGCTCGGC	GGGTCTGATG	GTGGCGGGCG	600
CTTGCGGCTA	TGTGGGCTGG	ATGAGCCTCA	CGCGCGGGCA	GGCGAGCTG	ACCGCGCGCC	660
AGGTCCGGGT	TGTTGCGGCG	GCTTACGAGA	CGGCTATGG	GCTGACGCTG	CCCCCGCGCG	720
TGATCGCCGA	GAACTGTGCT	GAACTGATGA	TTCTGATAGC	GACCAACCTC	TGGGGGCAAA	780
ACACCGCGGC	GATCGCGGTC	AACGAGGCGG	AATACGCGCA	GATGTGGGCT	CAAGACGCGG	840
CGCGGATGTT	TGCTACGCG	GCGCGGACCG	CGACGCGGAC	CGGACGTTG	CTGCGGTTCC	900
AGGAGGCGGC	GGAGATGACC	AGCGCGGGTG	GGCTCTCTGA	GCAGGCGCGC	GCGGTGAGGC	960
AGGCTCTCGA	CACCGCGCGG	GCGAACCAGT	TGATGAACAA	TGTGCCCCAG	GCGCTGCAAC	1020
AGCTGGCCCC	GCCACGCGAG	GGCACGCGCG	CTTCTTTCCAA	GCTGGGTGCG	CTGTGGAAGA	1080
CGGTCTCGCG	GCATCGGTGG	CGGATCAGCA	ACATGCTGTC	GATGCGCAAC	AACCACATGT	1140

CGATGACCAA	CTCGGCTGTG	TCGATGACCA	ACACCTTGAG	CTCGATGTTG	AAGGGCTTTG	1290
CTCGGCGCGC	GGCGCCCCAG	GGCGTGCAAA	CGCGCGGCGA	AAACGGGGTC	CGGGCGATGA	1260
GCTCGCTGGG	CAGCTCGCTG	GCTTCTTCCG	GTCTCGGCGG	TGGGCTGGCC	GCCAACTTGG	1320
GTGGGGCGGC	CTCGGTGGGT	TGTTTGTCCG	TGCGCGAGGC	CTGGGCGCGG	GCCAAACAGG	1380
CACTCACCCC	GGCGGCGCGG	GCGCTGCGGC	TGACCAAGCT	GACCAAGCGC	GCGGAAGAG	1440
GGCGCGGCGA	GATGCTGGGC	GCGCTGCGGC	TGGGCGAGAT	GGCGCGCAGG	GCGGCTGGTG	1500
GCGTCACTGG	TGTGCTGGGT	GTTGCGCGGC	GACCGTATGT	GATGCGCGAT	TCTCGCGCGG	1560
CGCGCTAGGA	GAGGGGCGGC	AGACTGTCTT	TATTTGACCA	GTGATCGCGG	GTCTCGGTGT	1620
TTCGGCGGCG	GCGTATGACA	ACAGTCAATG	TGCATGACAA	GTTACAGGTA	TTAGGTCCAG	1680
GTTCAACAAG	GAGACAGGCA	ACATGGCGTC	ACGTTTTATG	ACCGATCGCG	ACCGGATGCG	1740
GGACATGGCG	GGCGGTTTTG	AGTGCACGCG	CCAGACGGTG	GAGGACGAGG	CTCGCGGGAT	1800
GTGGGCGCTC	GCGCAAAACA	TTTCCGGTGC	GCGCTGGAGT	GCGATCGCGG	AGCGGACCTC	1860
GCTAGACACC	ATGGGCGCAG	TGAATCAGGC	GTTTCGCGAC	ATCGTGAACA	TGCTGCACGG	1920
GCTGGGTGAC	GGGCTGGTTC	GCGACGCGCA	CAACTACGAG	CAGCAAGAGC	AGGCTTCCCA	1980
GCGATCGCTC	AGCAGCTAAC	GTCAGCGGCT	GCGGCACAA	ACTTTTACAA	GCGAGGAGAA	2040
ACAGGTTGCA	TGACCATCAA	CTATCAATTC	GCGGATGTGG	ACGCTCAGCG	CGCGATGATC	2100
CGCGCTCAGG	CGGGGTTGCT	GGAGGCGGAG	CATCAGGCGA	TGATTCGTGA	TGTGTTGACC	2160
GCGAGTGACT	TTTGGGCGCG	CGCGGTTTCC	GCGGCGTGGC	AGGGGTTGAT	TACCGAGTTG	2220
GGGCTTAAT	TCCAGGTGAT	CTACGAGCAG	GCCAAAGCGC	ACCGGCGAGAA	GCTGCAGGCT	2280
GGCGGCAACA	ACATGGCGCA	AACCGACAGC	GGGCTGCGCT	CGAGCTGGGC	CTGACACCAG	2340
GCCAAAGGCA	GCGACGTGCT	GTACGAGTGA	AGTTCCCTGC	GTGATCCTTC	GCGTGGCAGT	2400
CTAAGTGCTC	AGTCTCTGGG	TGTTGGTGGT	TTGCTGCTTG	GCGGGTTCTT	GCGTCTGCTT	2460
CAGTCTGCTT	CGGGCTCGGG	TGAGGACCTC	GAGGCGCAGG	TAGCGCGCTC	CTTGGATCCA	2520
TTGCTGCTGT	TGTTGGGCGA	GGACGCGTCC	GACGAGGCGG	ATGATCGAGG	GCGGTCGGGG	2580
GAAGATGCCC	ACGAGCTCGG	TTGCGGCTCC	TACCTCTCGG	TTGAGGCGTT	CCTGGGGGTT	2640
GTTGGACCA	ATTTGGCGCC	AGATCTGCTT	GCGGAAGGCG	GTGAACGCGA	GCACTCGGCT	2700
GCGGCGGCTG	TGAGGTTGCT	GCGGACCGCG	GCGGAGTTTG	TGGGTCAGAG	CCTCGAGTAC	2760
GCGATCATAT	TGGGCAACAA	CTGATTCGCG	GTCGCGCTCG	TGATAGATGG	AGTGCAGCGG	2820

```

GCTGCGCACC CACGGCCAGG AGGCTTCGG GTTGGCTGCC ATCAGATTGG CTGCGTAGTG      2880
GGTTCTGCAG CCTGCCCAGG CCGCTCCGGG CAGGCTGGCG CCGATCGCG CCACCAGGCT      2940
GGCGTGGGCG TCGCTGGTGA CCAGCCGGAC CCGGACAGG CCGCGGGCGA CCAGGTGCG      3000
GAAGAAGCGG AGCAGCGCG CCGCTCTCTC GCGCGAGGTG ACCTGATGC CCAGGATC      3058

```

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
20           25           30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35           40           45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
50           55           60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65           70           75           80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
85           90           95
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
100          105          110
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
115          120          125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
130          135          140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
145          150          155          160
Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
165          170          175
Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
180          185          190

```

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu  
 195 200 205  
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu  
 210 215 220  
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn  
 225 230 235 240  
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val  
 245 250 255  
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala  
 260 265 270  
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala  
 275 280 285  
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly  
 290 295 300  
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val  
 305 310 315 320  
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg  
 325 330 335  
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly  
 340 345 350  
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly  
 355 360 365  
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met  
 370 375 380  
 Pro His Ser Pro Ala Ala Gly  
 385 390

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GACGTCAGCA CCGGCGGTGC AGGGCTGGAG CTTGCTGGGT TTGATCTGC GGTCAAGTC 60  
 AGCTGCTTCG GGTGTGCGC GCGGTGGATG CAGACTCGAT GCGGTCTTTT AGTGCACCTA 120  
 ATTTCGTTGA AGTGCCTGCG AGGTATAGGA CTTACCAATT GGTAAATGTA GCGTTCACCC 180

CGTGTTCGGG	TGGATTTGGC	CGSACCAGTC	GTACACCAAGC	CTTGCCCTGC	GCGCCAGGCG	240
GCGGATCAGA	TGCGTTGACT	ACCAATCAAT	CTTGAGCTTC	CGGGCCGATG	CTCGGCTAA	300
ATGAGGAGGA	GCACGCTGT	CTTTCACCTC	GCAACCGGAG	ATGTTGGCGG	CCCGGCTGG	360
CGAACTTCGT	TCCCTGGGGG	CAACCTGAA	GGCTAGCAAT	GCGGCCGAG	CCGTGCCGAC	420
GACTGGGGTG	GTGCCCCCGG	CTGCCAGGA	GCTGTGCTG	CTGCTTGCCA	CACAATTCG	480
TACGCATGCG	GCGACGTATC	AGACCGCCAG	CGCCAAGGCC	GCGGTGATCC	ATGAGCAGTT	540
TGTACACCG	CTGCCACCA	GCSCTAGTTC	ATATCCGAC	ACCGAGGCCG	CCACGCTGT	600
GCTCACCGGC	TAGCTCAGCT	GACCGTATTC	GACCGGAGG	ATTATCGAAG	TGCTGATTT	660
CGGGGCTTA	CCACCGGAGA	TCAACTCCGC	GAGGATGTAC	GCGGCGCGCG	CTTGGGCTTC	720
GCTGGTGGCC	GCGGCGAAGA	TGTGGGACAG	CGTGGCGACT	GACCTTTTTT	CGGCGGCTTC	780
GGCGTTTCAG	TGGTGGTCT	GCGGTCTGAC	GCTGGGCTCG	TGGATAGCTT	CGTGGCGCGG	840
TCTGATGGCG	GCGGCGGCTT	CGCCGATGT	GCGGTGGATG	AGCGTCAAGC	CGGGGCGGCG	900
GCAGCTGACC	GCGGCGGAGG	TCCGGTTTC	TCCGGCGGCG	TACGAGACAG	CGTATAGGCT	960
GACGTTGCCC	CGGCGGCTGA	TGCGGAGAA	CGGTACGAA	CTGATGACGC	TGACCGGAC	1020
CAACCTCTTG	GCGCAALACA	GCGCGCGGAT	CGAGGCCAAT	CAGGCGGAT	ACAGCCAGAT	1080
GTGGGGCCAA	GACGCGGAGG	CGATGTATGG	CTACCGCGCG	ACGCGCGGCA	CGGCGAGGCA	1140
GGCGTTGCTG	CGTTGCGAGG	ACGCGCTACT	GATCAGCAAC	CGCGCGGCGC	TGCTTACGCA	1200
GCGCGTCCCG	GTGAGGAGG	CCATCGACAC	CGCGCGGCGC	AACGAGTTGA	TGAACAATGT	1260
GCGCGAGGCG	GTGCAACAGC	TGCGCTAGCC	AGCGCAGGCG	GTGCTACCTT	CTTCCAAGCT	1320
GCGTGGGCTG	TGGAGCGCGG	TCTGCGGCGA	TCTGTGCGCG	CTCAGCAAGC	TCACTTCGAT	1380
AGCCAAACAAC	CACATGTGCA	TGATGCGCAC	GCGTGTGTCT	ATGACCAACA	CCTTGCACTC	1440
GATTTTGAAG	GCGTTAGCTC	CGCGCGGCGC	TCAGGCGGCT	GAAACCGCGG	CGGAAACCGG	1500
GCTGTGGGCG	ATGAGCTGCG	TGCGCAGCCA	GCTGGGTTCT	TGCGTGGGTT	CTTGGGTTCT	1560
GGGCGGTCGG	GTGGCGGCGA	ACTTGGGTCG	GCGCGGCTCG	GTGCGTTCTT	TGTGGGTCGC	1620
GCGAGCATCG	GCGCGGCGCA	ACGAGGCGGT	CACCGCGCGC	GCGCGGCGCG	TGCGGCTGAC	1680
CAGCGTGACC	AGCGCGGCGC	AAACCGCGCG	CGGACACATG	CTGGG		1725

(2) INFORMATION FOR SEQ ID NO:104:

(1) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 359 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1           5           10           15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20           25           30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35           40           45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
50           55           60
Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65           70           75           80
Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
85           90           95
Ala Tyr Gln Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
100          105          110
Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
115          120          125
Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
130          135          140
Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
145          150          155          160
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
165          170          175
Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Gln Ala Ile
180          185          190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
195          200          205
Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
210          215          220
Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
225          230          235          240
Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
245          250          255

```

Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala  
 260 265 270  
 Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met  
 275 280 285  
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu  
 290 295 300  
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser  
 305 310 315 320  
 Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro  
 325 330 335  
 Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr  
 340 345 350  
 Ala Pro Gly His Met Leu Gly  
 355

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ACTTCAGTGG AGAATGATAC TGAGGGGCTG TATCCACGAT GGCTGAGACA ACCGACCCAC 60  
 CCGCGGACGC GGGGACATCG CAAGCCGACC CGATGGGCTT GCGCGCCGAA GCGGAAGCCC 120  
 CCGAAGCCGA AGCGCTGGCC GCGCGGGCCC GGGCGGCTGC CCGTGCCGCC CCGTTGAAGC 180  
 GTGAGGCGCT GCGGATGGCC CCAGCCGAGG ACCGAGAAGT CCGCGAGGAT ATCGAGACTG 240  
 GGAAGACGCC GAAGACTATG ACCACTATGA CGACTATGAG GCGCGAGACC AGGAGGCCGC 300  
 ACGGTGGGCA TCGTGGCGAC GGGGCTGGCC GGTGCGCTTA CCAAGACTTT CCACGATTGC 360  
 CATGGCGGCT CGAGTCCTCA TCACTGCGCG CTTCACCGGG CTCAGCGGAT ACATTGTGTC 420  
 GCAACACCAT GAGGCCACCG AACGCCAGCA GCGCGGCGCG GCGTTGCGCG CCGGAGCCAA 480  
 GCAAGGTGTC ATCAACATGA CCGCGCTGGA CTTCAACAAG GCGGAAGGAG ACCTGCGCGC 540  
 TGTGATCGAC AGCTCCACCG GCGAATTGAG GGATGACTTC CAGCAGCGCG CAGCCGATTT 600  
 CACCAAGGTT GTCGAACAGT CCAAACTGGT CACCGAAGGC ACCTGACCG CACAGCCGTT 660  
 CGAATCCATG AACGAGCATT CCGCCGTGCT GCTCGTGGCG GCGACTTCAC GCGTCACCAA 720

TTCCGCTGGG	GCGAAAGAGG	AACCACGTGC	GTGGCGGCTC	AAAGTGACCG	TGACCGAAGA	780
GGGGGACAG	TACAAGATGT	CGAAAGTTGA	GTTCGTACCG	TGACCGATGA	CGTACGCGAC	840
GTCAACACCG	AAACCACTGA	CGCCACCGAA	GTGGCTGAGA	TGACTCAGC	CGCAGGCGAA	900
GGCGGTGATT	CGGCGACCGA	GGCATTGTAC	ACCGACTCTG	CAACCGAATC	TACCGCGCAG	960
AAGGGTCAGC	GGCACCTGA	CCTGTGGCGA	ATGCAGGTTA	CCTTGAAACC	CGTTCCGCTG	1020
ATTCTCATCC	TGCTCATGTT	GATCTCTGGG	GGCGCGACCG	GATGGCTATA	CCTTGAGCAA	1080
TACGACCCGA	TGAGCAGAGC	GACTCCGGCG	CGCGCCGTGC	TGCCGTCCGC	GGCGGCTCTG	1140
ACGGGACAAAT	CGCGCTGTTG	TGTATTCCAC	CGACACGTGG	ACCAAGACTT	CGTACCGCC	1200
AGGTCCGACC	TGCGCGCGGA	TTTCCTGTCC	TATACGACCA	GTTCACGCG	CAGATCGTGG	1260
CTCGCGCGGC	CAAACAGAAAG	TCACTGAAA	CGACCGCGAA	CGTGGTCCGC	CGCGCCGTGT	1320
CGGAGCTACA	TCCGGATTGG	GCCGTGGTTC	TGGTTTTTGT	CGACGAGAGC	ACTACCAATA	1380
AGGACAGCCC	CAATCCGTGG	ATGGCGGCCA	GCAGCGTGAT	GGTGACCCTA	GCCAAGGTGG	1440
ACGGCAATTG	GCTGATCACC	AAGTTCACCC	CGGTTTAGGT	TGCCGTAGGC	GSTCGCCAAG	1500
TGTGACGGGG	GGCGGGGTGG	CTGCTGGTGC	GAGATACCGG	CGTTCTCCG	GACAAATCAG	1560
GGCGGACCTC	AAACAGATCT	CGGCGGCTGT	CTAATCGGCG	CGTTATTATA	AGATTAGTTG	1620
CCACTGTATT	TACCTGATGT	TCAGATTGTT	CAGCTGGATT	TAGCTTCGCG	GCAGGGCGGC	1680
TGGTGCACCT	TGCATCTGGG	GTTGTGACTA	CTTGAGAGAA	TTTGACCTGT	TGCCGACGTT	1740
GTTCGCTGTC	CATCATTTGT	GCTAGTTATG	GCCGAGCGGA	AGGATTATCG	AAGTGGTGGA	1800
CTTCGGGGCG	TTACCAACCG	AGATCAACTC	CGCGAGGATG	TACGCGCGCC	CGGTTTGGGC	1860
CTCGCTGGTG	GGCGCGCGGA	AGATGTGGGA	CAGCGTGGCG	AGTGACCTGT	TTTCGGCGGC	1920
GTGCGGCTTT	CAGTCGGTGG	TGTGGGGTCT	GACGACCGGA	TGGTGATAG	GTTCGTGGGC	1980
GGGTCTGATG	GTGGCGGGCG	CCTCGCCCTA	TGTGGCGTGG	ATGAGCGTCA	CGCGGGGCGA	2040
GGCGGAGCTG	ACCGCGCGCC	AGGTCGGGCT	TGCTCGGGCG	GGTACCGAGA	CGCGGTATCG	2100
GCTGACGGTG	CGCGCGCGCG	TGATCGCGGA	GAACCGTGCT	GAACTGATGA	TTCTGATAGC	2160
GACCAACCTC	TTGGGGCGAA	ACACCGCGGC	GATCGCGGTC	AACGAGGGCG	AATACGGGGA	2220
GATGTGGGCT	CAAGAGCGCG	CGCGGATGTT	TGGCTAGCGC	GCCACGGCGG	CGACGCGGAC	2280
CGAGGCGTTG	CTGCGGTTGG	AGGACGCGCC	ACTGATCAGC	AACCGCGCGG	GGCTCGTTGA	2340
GCAGGCGCTC	GGGTCGAGG	AGGCGATCGA	CAGCGCTCGG	GCGAACCAGT	TGATGAACAA	2400

```

TGTGCCCCAA GCCTGCAAC AACTGGCCCA GCCACGAAA AGCATCTGGC CTTTCGACCA      2460
ACTGAGTGAA CTCTGGAAG CCATCTGCC CCATCTGTGG CCGCTCAGCA ACATCTGTTC      2520
GATGCTCAAC AACCACGTGT CGATGACCA CTGGGTGTGT TCGATGSCCA GCACCTTSCA      2580
CTCAATGTTG AAGGCTTTT CTCCGCGGGC GGCTCAGGCC GTGGAAACCG CGGCGCAAAA      2640
CGGGGTCCAG CGCATGAGCT CCTGCGCAG CCAGCTGGGT TCGTCGCTGG GTTCTTCGGG      2700
TCTGGGCGCT GGGGTGCCCC CCAACTTGGG TCGGGCGGCC TCGGTGCGTT CTTTGTGGT      2760
GCCCAGGCTT TGGCCCCGG CCAACCAGCC GGTACGCCCC GCGGCGCGGG CGCTGCGGCT      2820
GACGAGCCTG ACCAGCGCGG CCAAAACCG CCGCGACAC ATGCTGGCGG GGCTACCGCT      2880
GGGCGAAGTG ACCAATAGCG GCGCGCGGTT GCGCGCGGTT AGCAATGCGT TCGCGATGCC      2940
GCGCGCGGCG TACGTAATGC CCGGTGTGCC GCGCGCGCGG TAACGCGCAT CCGCAGCCAA      3000
TCCGCGCGCT CTATGCGCGC AGCGATC                                     3027

```

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1             5             10             15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20             25             30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35             40             45
Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50             55             60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65             70             75             80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Glu Val Arg Val Ala Ala Ala
 85             90             95
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
100             105             110
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly

```

115	120	125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met		
130	135	140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala		
145	150	155
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr		
	165	170
		175
Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile		
	180	185
		190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu		
	195	200
		205
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu		
	210	215
		220
Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn		
	225	230
		235
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val		
	245	250
		255
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala		
	260	265
		270
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met		
	275	280
		285
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu		
	290	295
		300
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser		
	305	310
		315
Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro		
	325	330
		335
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr		
	340	345
		350
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn		
	355	360
		365
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro		
	370	375
		380
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly		
	385	390
		395

(2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATCGGAGGG	AGTGATCACC	ATGCTGTGGC	ACGCAATGCC	ACCGGAGTAA	ATACCGCACS	50
GCTGATGGCC	GGCGCGGGTC	CGGCTCCAAAT	GCTTGCGGCH	GGCGCGGGAT	GGCAGACCTT	120
TTGCGCGGCT	CTGGACGCTC	AGGCGGTGGA	GTTGACCGCG	CGGCTGAACCT	CTCTGGGAGA	180
AGGCTGGACT	GGAGGTGGCA	GGGACAGGCG	GCTTGCGGCT	GCAACGCGCA	TGGTGGTCTC	240
GCTACAAACC	GGTCAACAC	AGGCAAGAC	CGGTGCGATG	CAGGCGACCG	CGCAAGCCGC	300
GGCATACACT	CAGGCGATGC	CGAGGACGCG	GTCGCTGGCG	GAGATCGGCG	CGAACCACAT	360
CACCCAGGCG	GTCCTTACGG	CGACCAACTT	CTTCGGTATC	AACAGGATCC	CGATCGGCTT	420
GACCGAGATG	GATTATTTCA	TGGTATGTG	GAACCAAGCA	GGCTGGGCAA	TGGAGGTCTA	480
CGAGGCGGAG	ACTGCGGTTA	ACAGGCTTTT	CGAGAGGCTC	GAGCGGATCG	CGTCGATCCT	540
TGATCGCGGC	GGAGCGGAGA	GGAGGACGAA	CCGATCTTTC	GGAATGCGCT	CGGCTGGCAG	600
CTCAACACCG	GTTGGCGGAT	TGCGCGCGGC	GGCTACCGAG	ACCTCGGCGC	AACTCGGTGA	660
GATGAGCGGC	CGGATCGAGC	AGTTGACCCA	GGCGCTGCAG	CAGGTGACCT	CGTTCTTCAG	720
CGAGGTGGGC	GGACCGCGCG	GGGCAACCC	AGCGGACGAG	GAAGCGCGCG	AGATCGGCTT	780
GCTCGGCACC	AGTCCGCTGT	CGAAGCATCC	GCTGCGTGGT	GGATCAGGCG	CGAGCGCGCG	840
CGCGGCGCTG	CTGCGCGCGG	AGTGGCTACC	TGGCGCAGGT	GGTCTGTTGA	CGCGCACGCC	900
GCTGATGTCT	CAGCTGATCG	AAAAGCGCGT	TGCGCGCTCG	GTGATGCGCG	CGGCTGCTGC	960
CGGATCTCTG	CGGACGCGTG	CGCGCGCTCC	GCTGGGTGCG	GGAGCGATCG	GCCAGGCTGC	1020
GCAATCGCGC	GGCTCCACCA	GGCGCGGCTT	GGTGGCGCGG	GGACGCTCG	CGCAGGAGCG	1080
TGAAGAAGAC	GACGAGGACG	ACTGGGACCA	AGAGGACGAC	TGGTGAGCTC	CGGTAATGAC	1140
AACAGACTTC	CGCGCGACCC	GGGCGCGAAG	ACTTGCCAAC	ATTTTGGCGA	GGAAGGTAAA	1200
GAGAGAAAT	AGTCCAGCAT	GGCAGAGATG	AAGACCGATG	CGGCTACCGT	CGCGCAGGAG	1260
GCAGGTAATT	TGGAGCGGAT	CTCGCGCGAC	CTGAAAACCC	AGATCGACCA	GGTGGAGTCC	1320
ACCGCAGGTT	CGTTGCAGGG	CGAGTGGCGC	GGCGCGCGCG	GGAGGCGCGC	CGAGGCGCGC	1380
GTGCTGCGCT	TGGAGGAAGC	AGGCAATAG	CAGAAGCAGG	AACTCGACCA	GATCTGAGC	1440

```

AATATTCTCTC AGGCCCCGCT CCAATACTCG AGGCCCCGACG AGGAGCAGCA GCAGCCGCTG      1500
TCTTCGCAAA TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG      1560
AGCAGCAGTG GAATTTCCCG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAAT      1616

```

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

CTAGTGGATG GGACCATGGC CATTTCTGCG AGTCTCACTG CTTCTGTGTG TGACATTTTG      60
GCAGCCCGGC GGAACCAAG CACTGGGGTC GAAGAACGGC TCGCTGCCA TATCTCCCG      120
AGTTCCATA CCTTCGTCCG GCGGAAGAG CTGTCTGTAG TCGGCGGCCA TGACAACCTC      180
TCAGATGCG CTCAAACCTA TAAACCTAG AAAGGGCGAG ACCGACGAA GGTGGAATC      240
GCGCGATCC GTCTTTCCT ATTCTACGCG AACTCGGCT TCGCTATGC GAACATCCCA      300
GTGACCTTC CTCCTGCGA AGCCATTGCC TGACCGGCTT CGCTGATCT CGCGCCAGG      360
TTCTGACCG CTTTCTTCAG CTCGCTAGCC GTGGCGTCC ATTTTCTCTG GACACCTCTG      420
TACCGCTCCG AA      432

```

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Leu Met      1
1           5           10           15
Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln      20
20          25          30
Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg      35
35          40          45
Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala      50
50          55          60

```

Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr  
 65 70 75 80  
 Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Ala Tyr  
 85 90 95  
 Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn  
 100 105 110  
 His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn  
 115 120 125  
 Thr Ile Pro Ile Ala Leu Thr Gln Met Asp Tyr Phe Ile Arg Met Trp  
 130 135 140  
 Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Gln Thr Ala Val  
 145 150 155 160  
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro  
 165 170 175  
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro  
 180 185 190  
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr  
 195 200 205  
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln  
 210 215 220  
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly  
 225 230 235 240  
 Gly Gly Asn Pro Ala Asp Gln Gln Ala Ala Gln Met Gly Leu Leu Gly  
 245 250 255  
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser  
 260 265 270  
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly  
 275 280 285  
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val  
 290 295 300  
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly  
 305 310 315 320  
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser  
 325 330 335  
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln  
 340 345 350  
 Gln Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp



355

360

365

## (2) INFORMATION FOR SEQ ID NO:110:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
1           5           10           15

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
20           25           30

Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
35           40           45

Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
50           55           60

Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
65           70           75           80

Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
85           90           95

Gln Met Gly Phe
100

```

## (2) INFORMATION FOR SEQ ID NO:111:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGCTCGAG TCGACGGCAG GTTCGTTGCA      60

GGCCCACTGG CCGCGCCCGG CCGGGACGGC CGCCAGGCC GCGGTGGTGC GCTTCCAAGA      120

AGCAGCCAAT AAGCAGAAGC AGGAACCGA CCAGATCTCG ACCAATATTC CTCAGGCCCG      180

GCTCCATATC TCGAGGGCCG ACCAGGAGCA GCAGCAGGCC CTGTCTCTCG AAATGGGCTT      240

CTGACCCGCT AATACGAAAA GAAACCGAGC AAAACATCGA CAGACGAGCA GTGGAATTTC      300

GGCGTATCTG AGGCTCCGGC AAGCCCATC CAGGGAATG TCAGCTCCAT TCATTCCCTC      360

```

CTTGACGAGG GGAAGCAGTC CTTGACCAAG CTCGCA

196

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala
1           5           10           15

Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
          20           25           30

Ala Ala Val Val Arg Phe Gln Gln Ala Ala Asn Lys Gln Lys Gln Glu
          35           40           45

Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
          50           55           60

Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
          65           70           75           80

```

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

GTGGATCCCG ATCCCTGTGT TCGCTATTCT ACCGGAATTC GGCCTTCCCG TATGCGAACA      60

TCCAGTGGAC GTTGCTTTCT GTCGAAGCCA TTGCTTGACC GGTTCGCTG ATCGTCCCG      120

CCAGTTCTG CAGCGCTTG TTGAGCTCG TAGCCCTGGC GTCCCATTTT TGCTGGACAC      180

CCTGGTACGC CTCGAACCG CTACCGCCCC AGCCGCTGC GAGCTTGGTC AGGACTGCT      240

TCCCCTGCTC AAGGAGGGAA TGAATGGAC TGACATTTC CTGGATTGCG CTTGCCCGCG      300

CCTCGATAAC CCGAAATTC CACTGCTGCT CTGTCACTT TTTGCTCGT TTCTTTTCT      360

ATTAGCGGTT CAGAAGCCCA TTTGCGA      187

```

## (2) INFORMATION FOR SEQ ID NO:114:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

CGGCACGAGG APTTGGGTTG GCCCAACGGC GCTGGCGAGG GCTCCCTTC GGGGGCGAGC      60
TCCGCGCCGG ATGCTTCCTC TGCCCGCAGC CGCGCTTCCA TGGATCGACC AGTTGCTACC      120
TTCCCSACGT TTCGTTGGGT GTCTGTGCGA TACCGGTGAC CCCGGCGGCG ACCTCGGGAG      180
TCTTGGGGGG CAGCCCGGGT CGCTGGTTCC GCCCGGCGAC CAGACGCTCT GGACCGGACC      240
GCCCGGGGTT CCGCGATTGG CATCTTTGCC CA                               272
  
```

(2) INFORMATION FOR SEQ ID NO:115:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val
1           5           10           15

Val Ala Ala Leu
                20
  
```

(2) INFORMATION FOR SEQ ID NO:116:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
1           5           10           15
  
```

(2) INFORMATION FOR SEQ ID NO:117:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys  
1                   5                   10                   15  
Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro  
1                   5                   10                   15

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Lys Ala Val  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ala Glu Glu Ser Ile Ser Thr Lys Glu Lys Ile Val Pro  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
1           5           10           15
Ser

```

## (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1           5           10           15

```

## (2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
1           5           10           15

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn
20           25           30

```

## (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro
1           5           10           15

Gly Gly Arg Arg Xaa Phe
20

```

## (2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Asp Pro Gly Tyr Thr Pro Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile  
1 5 10 15

Asn Val His Leu Val  
20

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

GCAACGCTGT CTTGCTTTT GCGTGATCG GTTTCGCTC GCTGCGGTG GCGGTGCGG    60
TCACCATCCG ACCGACCCG GCTTCAAAAC CGTAGAGCG ACACCAAAAC GCGCAGCCAG    120
GGAAGTTTAT GCGTTGTTG CCSACGCAAC ACCAGCGCC GGTCCCGCC GCTCGCCCG    180
ATGATCCGAC CGCTGGATC CAGCGCGCGA CCATTCCGC TGTACAGAAC GTGGTGGCG    240
GGCCCGGTAC CTCACCCCG GTGGGTGGGA CGCCGCTTC GCCTGCGCG GAAGCGCGCG    300
CGGTGCGCGG TGTGTGCTT GCGCGGTGC CAATCGCGT CCGGATCATC ATTCCCGCT    360
TCCCGCGTTC GCAGCTGGA ATGCGGACCA TCCCCACCG ACCCGCGAG ACGCGGTGA    420
CCACGTCCGC GACGACCGG CCGACCAAC CGCGGACAC GCGCGTGAAC ACCCGCCAA    480
CGACGCGCG GACGACCGG GTGACCAAC CGCAACGAC GCGCGCGAG ACCCGGTGA    540
CCACGTCAC AACGACCGT GCGCGGAGG CGTGGCGCG GACGACGTC GCTCGGACCA    600
CGTGGCGCG GACGACGTC GCTCGGAGG CGCGGACCG GACGACGTC GCTCGGAGG    660
CGACGCGCA GCGGAGGCA CAACCAACG AACAGATGG AACCGAGCG CAGACCGTGG    720
CGCGGCGAG GGTGGCGCG GCTCGGAGG CGCGGTCGG TGGCGGCAAC GCGGCGCGG    780
GGGCGGACTT ATTGGCGCG TTCTGATCAG GCTCGCGCT TCACTACGT CCGAGGACAT    840
GGCGGTGAT GCGGTGAGG TGGTGTGCG GTGTCTCAAC GA                882

```

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CCATCAACCA ACCGCTGCG CGGCGCGCGC CGCGCGATCC GCGGTGCGCG CCACGCTGCG	60
CGGTGCTGCG GGTGCGCGCG TTGCGCGCGT CGCGCGCGTC GCGCGCGACC GGTGCGGTGCG	120
CTAGCGCGCGT GTTACCGCGCG TCGTTGCGCG GACCGCGCGG GCGACCGCGG GTACCGCGCGA	180
TGGCGCGCGTT GCGCGCGCGG GACCGGTGCG CACCGTTGCG ACCGTGCGCA CGGTGCGCGA	240
CCACCGCACCG GCGCGCGACA CGCGCACCGC CGCGCGCGCG CGCACCGCGG CGGTGCGCGT	300
TGCTGCGCGT ACCGCGCGCA CGCGCGTTGCG CGCGGTGCGG GCGACCGGAA CTACCGCGCG	360
ACCGCGCGCTG CGCGCGCGCG CGCGCGCGAC CGCGATGCGG ACCGCGGTCA CGCGCGCGTG	420
GGAGTGCCTG GATTAGCGCA CTGACCGCGG CAACCGAGCGG AAGTACTGTC GTTACCGCGG	480
CAGTTCGAGA CGACCGACA GACCGCGGTG GTGCGCGGAC TGGGTGAAAT GCGACCGCAT	540
AGCGGTGAGC TGTGCGGTGCG GTTCAACGTC GATCATGATG TCGAGGTGAC CGTACCGCGG	600
CGCGCGGAGG GAGCGCGTGA ACTCGCGGTT GAGCGCGATG GCGATCGGTT GCGCGCGTGC	660
CCAGCGCAAT ACCGCGGATG CGCGGTGCGA AGCGCGCGCG AGCGCGGCTT CGGTGCGCGG	720
ACGTGCGTGC GGTGCGCGTG TTACCGCGTT GTGTCGGAAC ACCAGTAGCA GTTCTGCTGC	780
GCGGAGCGCA TCCACCGCGG GTTGCCTGAG CTCGT	815

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCAGCGCGG GGTGAGGTG TCAGATCAGA GAGTCTCGCG ACTCAGCGGG GCGGTTCAGC	60
CTTCTCCGAG AACAACTGCT GAAGATGCTC GCGCGCGAAA CAGGCGGTGA TTGACGCTC	120
TATGACCGGT TGAACGACGA GATCATCGCG CAGATTGATA TGGACCGCT GGGCTAACAG	180
GTGCGCAAGA TGGTGCAGCT GTATGCTGCG GACTCGGTGT CCGCGATCAG CTTTGCGGAC	240
GGCGCGGTGA TGTGTGAGAG CGAGGAGCTC GCGGAGAGCC AGTATCGGAT CGAGACGCTG	300
GACCGCATCA CGTTGTTTGG GCGCGCGACG ATGACAACCG CTTTCATGTT TGAGATGCTC	360
AAGCTTGAGC GCGACATCCA GTTCTTCAGG ACCGACCGCG ACTACCGGG CCGGATCTCA	420

ACACCCGACG TGTCTACGC GCCCGCGCTC CGTCAGCAAG TTCACCGCAC CGACGATCCT	480
GCGTTCTGCC TGTCTTAAG CAGCGGATC GTCTCGAGGA AGATCCTGAA TCAGCAGGCC	540
TTGATTGGG CACACACCTC GGGGCAAGAC GTTCTGAGA GCATCCGCAC GATGAAGCAC	600
TGGCTGGCT GGGTCGATCG ATCGGGCTCC CTGGCGGAGT TGAACGGTT CAGGGGAAT	660
GCGGCAAGG CATACTTAC CGCGCTGGG CATCTCTCC CACAGGAGT CGCATTCCAG	720
GGCGCTCGA CTCGGCGCC GTTGGAGCC TTCAACTCGA TGGTCAGCCT CGCTATTCC	780
CTGCTGTACA AGAACATCT AGGGCGGATC GAGCGTCACA GCTTGAACGC GTATATCGGT	840
TTCTACACC AGGATTACG AGGGCAGCG ACCCTCTCTG CGGAATTCCG CAGGAGCTCC	900
GCTGAAACCG CTGGCGGCT GCTCAGTCC GTACCTAAT CGGCTGCGC CAGGCGGCT	960
CGCGGCGCGA ATACCAGCAG ATCGGACAG GAATTCCCG CAGCGCGTT GGAGCGCTCC	1020
ATACCGCGG CACACTCAC GCGAGCGAAC AGGCTTGCGA CCGTGCGCG GCGGCTCTCC	1080
GGCTCTACTT CGACCGCGC CATCAGCTAG TCACAGCTCG GCGGACTTC CATTGCGTCC	1140
GTTCGGCAG AG	1152

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTCGTCCGA TTGGCAGGG TGTACTTCCC GGTGGTGTAN GCCGATGAG TCCGACGAC	60
CAGCAATGCC GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGTCCA GTGGGCGAT	120
CGGCTCGAGT CCGCGCTGG CGGCTCTTTC CTTCGGCAGG CTCATCCGAC GTTTTCCGC	180
CGTGGTTTTC CGCATTATG CCGGCGCGCC GCCTCGGGCG GCGGTATGG CGGAANETCG	240
ATCAGCACAC CGAGATACG GGTCTGTGCA AGCTTTTGA GCTTCGCGG GGCAGCTTC	300
GCGGCAATT CTACTAGCGA GAAGTCTGG CCGATACCGA TGTGACCGA GTGGTGGCG	360
TGCAGCCAC CTTATTGCC GATGGCGCG ACCATGCGC CTGGACCGAT CTTGTGCGC	420
TTCCGACCG CGACCGGTA GGTGGTCAAG TCGGTCTAC GCTTGGGCT TTCCGACCG	480

```

TCCCGACGCT GGTCCCGGTT GCGCCCGGAA AGCCSCGGGT CCGGTGCCAT CAGGAATGCC      540
TCACCCCCGC GGCACGAC GGCACGAC GCGCGATGT CAGCATCGG GACATCATGC      600
TCGCTTCAT ACTCTCGAC CAGTCGCGG AACACCTGGA TTCCCGGACC GCGCA      655

```

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
1           5           10           15
Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu
20           25           30
Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
35           40           45
Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Asp Asp Pro Thr Ala
50           55           60
Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
65           70           75           80
Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
85           90           95
Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
100          105          110
Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
115          120          125
Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
130          135          140
Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr
145          150          155          160
Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
165          170          175
Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
180          185          190
Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro

```

195	200	205
Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro		
210	215	220
Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala		
225	230	235 240
Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn		
245	250	255
Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe		
260	265	

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro		
1	5	10 15
Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro		
20	25	30
Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu		
35	40	45
Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro		
50	55	60
Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr		
65	70	75 80
Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro		
85	90	95
Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser		
100	105	110
Pro Pro Thr Gln Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro		
115	120	125
Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile		
130	135	140
Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala		
145	150	155 160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly  
 165 170

## (2) INFORMATION FOR SEQ ID NO:139:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly  
 1 5 10 15  
 Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg  
 20 25 30  
 Asn Arg Arg  
 35

## (2) INFORMATION FOR SEQ ID NO:140:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu  
 1 5 10 15  
 Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr  
 20 25 30  
 Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu  
 35 40 45  
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala  
 50 55 60  
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp  
 65 70 75 80  
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala  
 85 90 95

Gly Gln Leu Arg Arg Gln Phe Tyr  
100

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCATAT GGGCCATCAT CATCATCATC ACCTCATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PCR Primer"
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CCTGATTTCA GGGCTCGGTT GGGGGGGGCT CATCTTGAA C GA

42

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PCR Primer"
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTCTGAATTC AGCGCTGGAA ATCCTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GGATCCAGCG CTGAGATGAA GACCTATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mycobacterium tuberculosis
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAGAGAATTC TCAGAAGCCC ATTGCGAGG ACA

33

## (3) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1991 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 182..1273

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

TGTTCCTTCGA CCGCAGGCTG GTGGAGGAAG GGGCCACCGA ACAGCTGTTC TCCTGCGCGA      60
AGCATGCGCGA AACCGCCCGA TAGCTGCGCG GACTGTGCGG GGAAGTCAAG GACGCCAAGC      120
GCGGAAATTC AAGAGCACAG AAAGGTATGG C GTG AAA ATT CST TTG CAT ACC      172
                               Val Lys Ile Arg Leu His Thr
                               1           5

CTG TTG GCG GTG TTG ACC GGT GCG CCG CTG CTG CTA GCA GCG GCG GCG      220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly
      10           15           20

TGT GCG TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC      268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala
      25           30           35

GGT ACT GTC GCG ACT ACC CCG GCG TCG TCG CCG GTG ACC TTG GCG GAG      316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu
      40           45           50           55

ACC GGT AGC ACC CTG CTC TAC CCG CTG TTC AAC CTG TCG GGT CCG GCC      364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala
      60           65           70

TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT      412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Glu Gly Thr Gly
      75           80           85

TCT GGT GCG GCG ATC GCG CAG GCC GCC GCG GCG ACG GTC AAC ATT GGG      460
Ser Gly Ala Gly Ile Ala Glu Ala Ala Ala Gly Thr Val Asn Ile Gly
      90           95           100

GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GCG      508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly
      105           110           115

```



CTG	ATG	AAC	ATC	GCG	CTA	GCC	ATC	TCC	GCT	CAG	CAG	GTC	AAC	TAC	AAC	536
Leu	Met	Asn	Ile	Ala	Leu	Ala	Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	
120					135					130					135	
CTG	CCC	GGA	GTC	AGC	GAG	CAC	CTC	AAG	CTG	AAC	GGA	AAA	GTC	CTG	GCG	604
Leu	Pro	Gly	Val	Ser	Glu	His	Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	
				140				145						150		
GCC	ATG	TAC	CAG	GGC	ACC	ATC	AAA	ACC	TGG	GAC	GAC	CCG	CAG	ATC	GCT	682
Ala	Met	Tyr	Gln	Gly	Thr	Ile	Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	
			155				160						165			
GCG	CTC	AAC	CCC	GGC	GTC	AAC	CTG	CCC	GGC	ACC	GCG	GTA	GTT	CCG	CTG	700
Ala	Leu	Asn	Pro	Gly	Val	Asn	Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	
	170						175					180				
CAC	GCG	TCC	GAC	GCG	TCC	GCT	GAC	ACC	TTC	TTC	TTC	ACC	CAG	TAC	CTG	748
His	Arg	Ser	Asp	Gly	Ser	Gly	Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	
	185					190					195					
TCC	AAG	CAA	GAT	CCC	GAG	GCC	TGG	GCC	AAG	TGG	CCC	GCG	TTC	GCG	ACC	796
Ser	Lys	Gln	Asp	Pro	Glu	Gly	Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	
200					205					210					215	
ACC	GTC	CAC	TTC	CCG	GCG	GTC	CCG	GCT	GCG	CTG	GCT	GAG	AAC	GCG	AAC	844
Thr	Val	Asp	Phe	Pro	Ala	Val	Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	
				220				225						230		
GCG	GCG	ATG	GTC	ACC	GCT	TGC	GCC	GAG	ACA	CCG	GCG	TGC	GTC	GCC	TAT	892
Gly	Gly	Met	Val	Thr	Gly	Cys	Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	
			235				240						245			
ATC	GCG	ATC	AGC	TTC	CTC	GAC	CAG	GCC	AGT	CAA	CCG	GGA	CTC	GCG	GAG	940
Ile	Gly	Ile	Ser	Phe	Leu	Asp	Gln	Ala	Ser	Gln	Arg	Gly	Leu	Gly	Glu	
	250						255					260				
GCC	CAA	CTA	GCC	AAT	AGC	TCT	GCG	AAT	TTC	TTC	TTC	CCC	GAC	GCG	CAA	988
Ala	Gln	Leu	Gly	Asn	Ser	Ser	Gly	Asn	Phe	Leu	Leu	Pro	Asp	Ala	Gln	
	265					270					275					
AGC	ATT	CAG	GCC	GCG	GCG	GCT	GCC	TTC	GCA	TGG	AAA	ACC	CCG	GCG	AAC	1036
Ser	Ile	Gln	Ala	Ala	Ala	Ala	Gly	Phe	Ala	Ser	Lys	Thr	Pro	Ala	Asn	
280					285					290					295	
CAG	GCG	ATT	TGG	ATG	ATC	GAC	GCG	CCC	GCC	CCG	GAC	GCG	TAC	CCG	ATC	1084
Gln	Ala	Ile	Ser	Met	Ile	Asp	Gly	Pro	Ala	Pro	Asp	Gly	Tyr	Pro	Ile	
			300					305						310		
ATC	AAC	TAC	GAG	TAC	GCC	ATC	GTC	AAC	AAC	CCG	CAA	AAG	GAC	GCC	GCC	1132
Ile	Asn	Tyr	Glu	Tyr	Ala	Ile	Val	Asn	Asn	Arg	Gln	Lys	Asp	Ala	Ala	
			315				320						325			
ACC	GCG	CAG	ACC	TTC	CAG	GCA	TTT	CTG	CAC	TGG	GCG	ATC	ACC	GAC	GCG	1180
Thr	Ala	Gln	Thr	Leu	Gln	Ala	Phe	Leu	His	Trp	Ala	Ile	Thr	Asp	Gly	

330	335	340	
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC			1228
Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
GCG CTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC			1273
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAGCCTCGTT GACCACCAGC CGACAGCAAC CTCGGTCGGG CCATCGGGCT GCTTTCGGGA			1333
GCATGCTGGC CCGTGGCGT GAAGTCGGCC GCGTGGCCC GCCCATCCG TGTTTGGGTG			1393
GGATAGGTTC GTGATCCCG CTGCTTCCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG			1453
AGGCGATGGG TCGATCAGG CTCACCGGCT TGCATTCTT CACCGCCACT GAATCGAATC			1513
CAGGCAACAC CTACCGCGAA ACCCTTGTCA CCGACGCTC GCCCATCCG TCGCGCGCTA			1573
CTACGCGCG TTGCGGTGA TCGTCGGAC GCTGGCGACC TCGGCAATCG CCGTATCAT			1633
CGCGTCCCG GTCTCTGTAG GAGCGCGCT GTGATCTTG GAACGGCTGC CGAAGCGTT			1693
GGCGAGGCT GTGGGAATAG TCGTGAATT GCTCGCGGA ATCCCCAGCG TGGTGGTCGG			1753
TTGTGGGGG GCAATGAGT TCGGCGCTT CATCGCTCAT CACATCGCTC CCGTATCGC			1813
TCACAACGCT CCGATGTGC CCGTCTGAA CTACTTCGC GCGACCCCG GCAACCGGGA			1873
GGGLATGTT GTTCCGCTC TCGTCTTGGC GTGATGCTC GTTCCATTA TCGCCACCAC			1933
CACTCATGAC CTGTTCCGCG AGTGGCGGT GTTGGCCCG GAGGCGCGGA TCGGGAATTC			1993

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Val	Lys	Ile	Arg	Leu	His	Thr	Leu	Leu	Ala	Val	Leu	Thr	Ala	Ala	Pro
1				5					10					15	
Leu	Leu	Leu	Ala	Ala	Ala	Gly	Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser
			20					25					30		
Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser
			35				40					45			
Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu

50	55	60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr 65 70 75 80		
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala 85 90 95		
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly 100 105 110		
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser 115 120 125		
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys 130 135 140		
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr 145 150 155 160		
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro 165 170 175		
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr 180 185 190		
Phe Leu Phe Thr Glu Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly 195 200 205		
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly 210 215 220		
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu 225 230 235 240		
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala 245 250 255		
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn 260 265 270		
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe 275 280 285		
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro 290 295 300		
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn 305 310 315 320		
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu 325 330 335		
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val 340 345 350		

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu  
 355 360 365

Ile Ala Thr Ile Ser Ser  
 370

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TGTTTCTTCCA	CGGCGAGGCTG	GTGGAGGAAG	GGCCCLACCGA	ACAGCTGTTT	TCCTCGCCCA	60
AGCATCCCGA	AACCGCCCCA	TACGTCCCGG	GACTGTCCGG	GGACGTCAAG	GACGCCAAGC	120
GGCGAAATTG	AAGAGCACAG	AAAGGTATGG	CGTGAAATTT	CGTTTGCATA	CGCTGTTGGC	180
CGTGTGACC	GCTGCGCCCG	TCCTGCTAGC	AGCGGCGGGC	TGTGGCTCGA	AACCACCGAG	240
CGTTTGGCT	GAAAGCGGCG	CGGCGCCCGG	TACTGTCCGG	ACTACCCCGG	CGTGTGCGCC	300
GCTGACCTTG	GCGGAGACCG	GTAGCACGCT	GCTGTACCGG	CTGTTCAACC	TGTGGGTGCC	360
GGCCTTTTCA	GAGAGGTATC	CGAAGTCAAC	GATCACGCTT	CAGGCGACCG	GTTGTGCTGC	420
CGGGATCCCG	CAGGCGCCCG	CGGCGACGCT	CAACATTGGG	GCTTCCGACG	CCTATCTGTC	480
GGAAGGTGAT	ATGGGCGCGC	ACAAGGCGCT	GATGAACATC	GGGCTAGCCA	TCTCGGTCCA	540
GCAGGTCAAC	TACAAGCTGC	CGGAGTGAAG	CGAGCACCTC	AAGCTGAACG	GAAAAGTCTT	600
GGCGGCCGAT	TACGAGGGCA	CGATCAAAAC	CTGGGACGAC	CGCAGATCG	CTGCGCTCAA	660
CCCCGGCGTG	AACCTGCCCC	GCAGGCGGCT	AGTTCCGCTG	CACCGCTCCG	ACCGGTCCGG	720
TGACACCTTC	TTGTTCACCC	AGTACCTGTC	CAAGCAAGAT	CCGAGGCTCT	GGGCAAGTTC	780
GGCCCGGCTTC	GGCAGCACCG	TGCACTTCCC	GGCGGTGCCC	GCTGCGCTCG	GTGAGAACGG	840
CAACGGCGCG	ATGGTGACCG	GTTCGCGCGA	GACACCGGGC	TGCCTGCTCT	ATATCGGCAT	900
CAGCTTCCTC	GACGAGGCGA	GTGACCGGGG	ACTCGGCGAG	GCCCAACTAG	GCAATAGCTC	960
TGGCAATTTC	TTGTTGCCCC	AGGCGCAAAG	CATTCAAGCC	GGCGCGGCTG	GCTTCGCATC	1020
GAAAACCCCC	GCGAACCAGG	CGATTTGGAT	GATCGACGGG	CCCGCCCCCG	ACGGCTACCC	1080
GATCATCAAC	TACGAGTAGG	CGATCTTCAA	CAACCGGCGA	AAGGACGCGG	CCACCGCGCA	1140

```

GACCTTTCAG GCATTTCTGC ACTGCGCGAT CACCGACCGC AACAGGCGCT CTTTCTTCCA 1200
CCAGGTTTCAT TTCCAGCCGC TCCCGCCCGC GGTGGTGAAG TTGTCTGACC CTTTGATCCG 1260
GACGATTTCC AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCCTC GGGCCATCGG 1320
GCTGCTTTTC GCAGCATGCT GCGCCGTGCC GGTGAAGTCC GCCCGCTCG CCGCGCCATC 1380
CGGTGGTTTC GTGGGATAGT TCGGTGATC CCGCTGCTTC CGTGGTCTT GGTCTCTGTC 1440
GTCTCTGTCA TCAAGCGAT GGTTCGATC AGGCTCAACG GGTTCATTT CTTCACTGCC 1500
ACCGAATGGA ATCCAGGCAA CACCTACCGC GAAACCGTTG TCACCGACGC GTCCGCCATC 1560
CGGTCCGGGC CTACTACGGG GCTTTGCCGC TGATCTCCCG GACGCTGCGC ACCTCGGCAA 1620
TCCCGCTGAT CATCGCGTG CCGGTCTCTG TAGGACCGCG GCTGGTGATC GTGGACCGCG 1680
TCCGAAACG GTTGGCGAG GCTGTGGGAA TAGTCTTGA ATTCTCTGCC GGAATCCCCA 1740
GGTGTGTCTT CGTTTGTTC GGGGCAATGA CTTTCGGGCC GTTCATCGCT CATCAGTCC 1800
CTCGGTGAT CGCTCACAAC GCTCCCGATG TCCCGGTCTT GAACCTACTG GCGCGCGACC 1860
CGGGCAACCG GAGGCGCATG TTGTGTCCG GTCTGTGTCT GCGGTGATG GTCTTCCCA 1920
TTATCGCCAC CACCACTCAT GACCTCTTCC GGCAGGTGCC GTGTTCGCC CCGGAGGCGC 1980
CGATCGGGAA TTC 1993

```

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids.
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1           5           10           15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20           25           30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35           40           45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50           55           60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65           70           75           80

```

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala  
 85 90 95  
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly  
 100 105 110  
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser  
 115 120 125  
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys  
 130 135 140  
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr  
 145 150 155 160  
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro  
 165 170 175  
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr  
 180 185 190  
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly  
 195 200 205  
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly  
 210 215 220  
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu  
 225 230 235 240  
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala  
 245 250 255  
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn  
 260 265 270  
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe  
 275 280 285  
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro  
 290 295 300  
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn  
 305 310 315 320  
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu  
 325 330 335  
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val  
 340 345 350  
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu  
 355 360 365  
 Ile Ala Thr Ile Ser Ser

370

## (2) INFORMATION FOR SEQ ID NO:151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

GGTCTTGACC ACCACCTGGG TGTGGAAGTC GGTGCGCGGA TTGAAGTCCA GGTACTCTGT      60
GTGCGCGCGG GCGAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGTAGC GTTGACGGT      120
GTAGCGAAAC GCGAACGCGG CCGCGTTGGG CACCTTGTTC AGCGCTGATT TGCACAACAC      180
CTCGTGGAAG GTGATGCGGT CGAATTGTGG CGCGCGAAGC CTGCGGACCA GCGCGATCCG      240
CTGCAACCGG GCAGCGCGCG TCGTCAACGG GCATCGCGTT CACCGCGACG GCTTGCGCGG      300
CGCAACGCAT ACCATTATTC GAACAACGGT TCTATACCTT GTCAACGCTG GCGGCTACCG      360
AGCGCGCGAC AGGATGTGAT ATGCCATCTC TCGCGCGACA GACAGGAGCC AGGCGTTATG      420
ACAGCATTCG GCGTCGAGCC CTACGCGCAG CCGAGTACC TAGAAATCGC CGGGAAGCGC      480
ATGGCGTATA TCGACGAAGG CAAGGGTGAC GCCATCGTCT TTCAGCACGG CAACCGGACG      540
TGTGTTTACT TGTGGCGCAA CATCATGCGG CACTTGGAAG GGCTGGGCGG GCTGCTGGCC      600
TGGGATCTGA TCGGATGGG CGCTTCGAC AAGCTCAGCC CATCGGACC CGACCGCTAT      660
AGCTATGCGG AGCAACGAGA CTTTTTGTTC GCGCTCTGGG ATCGGCTCGA CCTCGCGGAC      720
CACGTGGTAC TCGTCTGCA CCACTGGGCG TCGCGGCTCG GCTTCGACTG GGCTAAGCAG      780
CATCGCGACC GAGTGCAGGG GATCGCGTTC ATGGAAGCGA TCGTCACCCC GATGACGTGG      840
GCGGACTGCG CCGCGGCGGT GCGGGGTGTG TTCCAGGGTT TCGGATCGCC TCAAGGCGAG      900
CGAATGCGGT TCGAGCACAA CATCTTTGTC GAACGGGTGC TCGCGCGGCG GATCTGCGA      960
CAGCTCAGCG ACGAGGAAAT GAACCACTAT CCGCGGCCAT TCGTGAACGG CCGCGAGGAC      1020
CGTGGCGGCA CGTTGTCTGT GCCACGAAAC CTTCCAATCG ACGGTGAGCC CCGCGAGGTC      1080
GTGCGCTTGG TCAACGAGTA CCGGAGCTGG CTGAGGAAA CCGACATGCC GAAACTGTTT      1140
ATCAACGCGG AGCGCGCGCG GATCATGACC GCGCGCATCC GTGACTATGT CAGGAGCTGG      1200
CGCAACCAGA CCGAATCAC AGTGGCGGCG GTGCATTTCT TTCAGGAGGA CAGCGATGCG      1260
GTGCTATCTT GCGCGCGGCG TCGCAGCAT CCGCGACCTG GGAGCGCTCT CATTTACGGA      1320

```

GACCAAGAAT GTGATTTCGG GCGAAGGCGG CGCCCTGCTT GTCAACTCAT AAGACTTCCT	1380
GCTCCGCGCA GAGATTTCGA GCGAAAAGGG CACCAATCGC AGCCGCTTCC TTCCCAACGA	1440
GGTCCACAAA TATACGTGGC AGGACAAAGG TCTTCCTATT TGCCACGCGA ATTAGTCGCT	1500
GCCTTTCTAT GGGCTCATT CGAGGAAGCC GAGCGGATCA CCGGTATCCG ATTGGACCTA	1560
TGGAACCGGT ATCATGAAAG CTTCGAATCA TTGGAACAGC GGGGGCTCCT GCGCCGTCCG	1620
ATCATCCGAC AGGGCTGCTC TCACAACGCC CACATGTACT ACGTGTACT AGCGCCGAGC	1680
GCCGATCGCG AGGAGTGCTT GCGCGCTCTG ACCAGCGAAG GTATAGGCGC GGTCTTTTAT	1740
TACGTGCGCG TTCACGATTC GCGCGCCCGG CCTCCT	1777

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAGATTGAAT CGTACCGGTC TCTTAGCGG CTCCTGCCG TGAATGCCCA TATCAGGCAC	60
GGCCATGTTT TGCTGTGGA CTTTGGCCCC ATGCCCGGAC GTTGGTAAAC CCAGGGTTTG	120
ATCAGTAATT CGGCGGACG GTTGGGGGAA GCGCGGACG ATGTGCTGA GCGCGGCGG	180
CGCCCTCGCC CAGCGGACCT CTGGATGCTC AGCCCGCGTG CGGCGACGTA GCGAGCGTT	240
CGCCCGTGTC GTCCACAGTG GTACTCGGT GACGACGCG CGCCGTGCTT GGGTGAAGAC	300
CGTGACCGAC GCGCGGATT CAGA	324

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1938 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GCGGTACGGC CGCTTTCGG TGGCACGGGA CTTGTAGGAC CTGAACCACT TGCCCTCGCG	60
AACGATTGAC GAACCGCTCG TGCGCGGCT GTGGGTGCTC AAGGTGTGGG GTGATGTCTT	120
CGATGACCGG CGCGGCACCG GCGCACTACG CGTGGAAGAC GTCTCGCGCG CCGGACGCGA	180



GCACGACTTC	CAGCCCGACT	CGATCGGCGT	GCTGACCGGT	CCTGTCGCTA	TGGCTGCTTG	240
GGAAGCTGCG	GTTCCGAAGC	GATTTGCGTT	GCTCACTGAC	CTCGACGCGC	ACGAGCAGCG	300
GTGGGCGGCG	TGCGACGAAC	GCCACCGCGC	CGAAGTGGAG	AACGCGCTCG	CGGTGCTGCG	360
GTCTGTATCA	ACCTGCGCGC	GATCGTGCGC	TTCCGCTGGC	ACGTTGCGCG	CTCGACCGCG	420
CTGAATCGAC	TAGATGAGAG	CAGTTGGGCA	CGAATCGGCG	TGTGCTGCTG	AGCAAGACAC	480
GAGTACTGTC	ATCACTATTC	GATGCACTGG	ATGACCGGCG	TGATTCAGCA	GGACCAATGG	540
AACTGCGCGG	GGCAAAACGT	CTCGGAGATG	ATCGGCGTCC	CCTCGGAACC	CTGCGGTGCT	600
GGCGTCATTC	GGACATCGGT	CGGCGTGGCG	GGATGCTGGT	GACGCGAGCG	CTGAAGGAGT	660
GGAGCGCGCG	GGTGACGCGC	CTGCTGGAGC	GGCGCGAGAC	GCTGCTGCTG	CGTAAGCGCG	720
GGATCGGCGA	GAAGCGCTTC	GAGGTGGCGG	GGACCGAGTT	CTTGTGCTTC	CGGACGCTCG	780
CGCACAGGCA	CGCGGAGCGG	GTTGCGCGCG	AGCACCGCGA	CCTGCTGCGC	CGGCGGCGCG	840
CGGACAGGAC	CGACGAGTGT	GTGCTACTGC	GGGCGCGAGC	GAAAGTTGTT	GCGGCACTGC	900
CGGTTAAGCG	GGACAGGGGT	CTGGACGCGA	TGAGGATCT	GCACATCTGG	ACCGCGGAGT	960
CGGTGCGCGC	CGACCGGCTC	GACTTTGCGC	CGAAGCAGAA	ACTGGCGGTC	TTGCTGCTCT	1020
CGGCGATGCG	GCTGGCGGAG	CGGTCGCGC	TGGCGGCTAG	GCGCGAGTAC	GGCGGTTGCA	1080
CGAGCTGGGT	GCAGCTGCGG	GTGACGCGCA	CTTTGGCGGC	GCGGCTGCAC	GACGAGGCGG	1140
CGCTGGCGCA	GGTCGCGGCT	CGGTCGCGG	AGCGCGTGCG	TTGACTGCGC	GGCATCGCTT	1200
GGGTCTGAGC	TGTACGCGCA	GTGCGCGCTG	CGAGTGATCT	GCTGTCGCTT	CGGTGCTGCG	1260
TGGGTCGAT	TGACGCGCGG	GGCAACAGCA	GCATTCGCGG	CGCCATCGTC	CGCGCGCGCG	1320
GGGCGGCTG	CTACAACG					1338

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CGGCGCGCAC	CGGCGGCAAC	GGCGGTACCG	GCGGCAACCG	CGGTGACGCG	GCTGCTGTGG	60
TGGGCTTGGG	CGCGAAGCGC	GACCGTGGCT	TGGCTGCGCG	CAAAGGCGGT	AACGCGCGAA	120
TAGGTGCGCG	CGCGGTGACA	GCGCGGCTCG	CGCGCGACCG	CGGCAACGCG	GGCAAGGCTC	180

```

GCACCGGCGG TCGCGCGCGG GCGGGCAACG ACCCGGCGAG CACCGGCAT CCGCGCGGTA      240
ACCGCGCGCA CCGCGCGGATC GCGCGTCCG GCGCGCGCGG CCGCGCGGCG GCACCGGCA      300
ACCGCGCGCA TCGCGGCAAC C                                          321

```

## (2) INFORMATION FOR SEQ ID NO:155:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

GAAGACCGGG CCGCGCGGATA TCGATCGGCT CCGCGACTAC TTTCGCGGAA CTGCGACGCG      60
CGCGCGTCCG GCTGATCATC ACCCGTGGCT ACAGCGCGAA CCGCACCGGA TGGCTGCTGC      120
CGTTGCGCTC CBAACTCGTC ACTTCGCGCG AGCGCGGACG GCACCGCGGA ATACCCAGCG      180
CGGTCCACGA TTGGGGTGCA AAGATCGTGC TGCAATCTCT GCACCGCGGA CGCTACGCTT      240
ACGACCGACT TCGGGTCAGC GCTTCGCGGA TCAAGCGCGC GATCAGCGCG TTTCGTCGCG      300
GAGCACTATC GCGTCGCGCG GTCGAAGCGA GCATCGCGGA TTTCGCGCGC TCGCGCGACT      360
TGGCGCGCGA TCGCGGCTAC GACGCGCTCG AATCATEGG CAGCGAAGCG TATCTGCTCA      420
ATCAGTTCTT CCGCGCGCGC ACCACAGAGC GCACCGACTC GTGGCGCGCG ACACCGGCGA      480
ACGTCGCGCG CT                                          492

```

## (2) INFORMATION FOR SEQ ID NO:156:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

She Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala
1           5           10           15

Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg
20           25           30

Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr
35           40           45

His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro

```

50	55	60
Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Gln 65 70 75 80		
Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys 85 90 95		
Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys 100 105 110		
Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu 115 120 125		
Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala 130 135 140		
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly 145 150 155 160		
Pro Asp Arg Tyr Ser Tyr Gly Gln Gln Arg Asp Phe Leu Phe Ala Leu 165 170 175		
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp 180 185 190		
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg 195 200 205		
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp 210 215 220		
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser 225 230 235 240		
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg 245 250 255		
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn 260 265 270		
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr 275 280 285		
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val 290 295 300		
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met 305 310 315 320		
Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg 325 330 335		
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val 340 345 350		

Pro Gly Val His Phe Val Glu Glu Asp Ser Asp Gly Val Val Ser Trp	335	360	363
Ala Gly Ala Arg Glu His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg	370	375	380
Asp Glu Glu Cys Asp Phe Arg Arg Arg Arg Arg Pro Ala Cys Glu Leu	385	390	400
Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Glu Gly Lys Gly His Glu	405	410	415
Ser Glu Pro Leu Pro Ser Glu Arg Gly Arg Glu Ile Tyr Val Ala Gly	420	425	430
Glu Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp	435	440	445
Ala Glu Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu	450	455	460
Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Glu Arg Gly Leu	465	470	475
Leu Arg Arg Pro Ile Ile Pro Glu Gly Cys Ser His Asn Ala His Met	480	485	490
Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala	500	505	510
Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu	515	520	525
His Asp Ser Pro Ala Gly Arg Arg	530	535	

(2) INFORMATION FOR GEO ID 00114.

## (1) SEQUENCE CHARACTERISTICS:

- ```

00 LENGTH: 204 amino acids
01 TYPE: amino acid
02 SEQUENCE:
03 TOPOLOGY: 1-chain

```

## (SEQ) SEQUENCE DESCRIPTION: SEQ IS NO. 1457.

Ser Gly Ser Ala Thr Arg Ser Pro Met Leu Thr Ser Ala Arg Pro Arg  
 10  
 Tyr Asp Ala His Ala Val Leu Leu Asn Gln Met His Ala Gly His Cys  
 20  
 Asp Thr Gly Leu Val Gly Pro Ala Pro Arg His Val Thr Asp Ala Ala  
 30

Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val  
 50 55 60  
 Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu  
 65 70 75 80  
 Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly  
 85 90 95  
 Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His  
 100 105 110  
 Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe  
 115 120 125  
 Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser  
 130 135 140  
 Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg  
 145 150 155 160  
 His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val  
 165 170 175  
 Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val  
 180 185 190  
 Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg  
 195 200 205  
 Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg  
 210 215 220  
 Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His  
 225 230 235 240  
 Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val  
 245 250 255  
 Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala  
 260 265 270  
 Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe  
 275 280

## (1) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ATGACATGT  | CCTCGGTGGT | GGTGCAGAG  | GCCTTTGCGC | GATTCGCGCG | CTACTCTTC  | 48  |
| GCCATGCAG  | CGATCGCCGG | TTTCTCCGAT | GCCTTGCGCC | AAGAGCTGCG | GGTAGCGGA  | 120 |
| ATCCCTCTCT | CGGTGATCCA | CCCGGCGCTG | ACCCAGACAC | CGCTGTTGCG | CAACGTCGAC | 180 |
| CCCCCGGACA | TCCCCCGGCC | GTTCGCGAGC | CTCACGCGCA | TTCCCGTTCA | CTGGGTCGCG | 240 |
| GCAGCGGTGC | TTGACCGTGT | GGCG       |            |            |            | 264 |

## (3) INFORMATION FOR SEQ ID NO:159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| TAGTCGCGCA | CGATGACGTC | GGGTTCCAGG | CCGACCGGCT | CAAGCACCAG  | CGCGACCACC | 60   |
| AAGCCCGTGC | GATCCTTACC | CGCGAAGCAG | TGGGTGAGCA | CCGCGCGTCC  | GGCGGCAAGC | 120  |
| AGTGTGACCA | CACGATGTAG | CGCGCGCTGT | GCTCCATTGC | GGTTGGGAA   | TTGGCGATAC | 180  |
| TGTTGCTTCA | TGTAGCGGT  | GGCGCGCTCA | TTTATCGACT | GGCTGGATTG  | CCCGGACTCG | 240  |
| CGTTGGAGC  | CGTCATTGCT | TAGCAGCTTC | TTGAATGCG  | TTTCTGCGCG  | CGCTGACTCG | 300  |
| TGGGCTCTAT | CATCGCGGAG | GTGGCGGAAC | GGCGGAGGCT | GGACCTCGAT  | GGCGTGGGAA | 360  |
| ACCGCTCTCG | GACCGCGCGG | GGCAACTTCT | CGGACGAGCC | GCAAGTGGCG  | AACGTCGCTC | 420  |
| ATCCCGAGCC | GGCGCAGCGT | TGCCCCCTCT | GGCGAATTGG | GCACGAGGCT  | GGCGAGCCAC | 480  |
| CGGCGATCAC | CAAGCAAGCG | TTGCGGAGTA | CGGATCGTCA | CTTCCGCGATC | CGGCGAGCCA | 540  |
| ATCTCTCTCG | CGGCGATCGT | CAGATCCCGC | TGCTGCGTTG | ACAAGAACCG  | CGGCGAGTGT | 600  |
| GCCAGCGGCT | ATCGGAGATT | GAACCGCGCA | CGCAGTTCTT | CAATCGCTTC  | GGCGTGGCGC | 660  |
| ACTATTGGCA | CTTTCGCGCG | GTGCGGCTAT | TCAGCAAGCA | TGCGAGTCTC  | GACGAACTCG | 720  |
| CCCCACGTAA | CCGACGCGCT | AGTCCCGCGC | GTGACCGCGA | CGATCGCGCG  | GTGATCTTTG | 780  |
| CGGCGACGCT | CGTAGCGGTT | GATCGACCGC | TTGCGCGTGC | CGGCGCGGAG  | CGCGATCAGC | 840  |
| TTATCGACCT | CGGCGTATGC | CGACGGCGAG | CTGGCGCGCT | TGCTCGAGGT  | CAAGAACTCC | 900  |
| ACCATCGGCA | CCGCGACCAA | GGTCCCGCAC | CTGACCTACG | TGCGCGAGCG  | CGACATCGCG | 960  |
| GAGTACAGCA | ACATCGCGCG | CTCGAGCGTG | TTCTTCAACT | ACGACGGTAC  | GTCCAACCGG | 1020 |

```

CGCACCACCG TCGTTTCGCA CBTACCGACT GGGTCCGACA CCATGTTTCT GGGCCCACTA 1088
ACCATCGGCG ACCGCGCGTA TACCGGGGCG GGCACAGTGG TCGCGGAGGA TGTCCGCGCG 1148
GGGCGCGCTGG CAGTGTGCGC GGGTCCGCAA C 1171

```

## (2) INFORMATION FOR SEQ ID NO:160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

GCAAAAGGCGG CACCGGCGGG GCGGGCATGA ACAGCTCGA CCGCTGCTA GCGGCGCAAG 60
ACGCGCGGCA AGCGGCGACC GCGGCGACCG GCGGCAACCG CCGCGCGCGC GGCACCACT 120
TCACCCAAAGG CCGCGACCGC AACGCGGCGA ACGCGGTGA CCGCGCGGTC GCGGCGAACC 180
GCGGAAACCG GCGAAACCGC GCAGACAACA CACCACTCG CCGCGCG 327

```

## (2) INFORMATION FOR SEQ ID NO:161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

CGTCCGCCACC ATGGCGCGGC AGGCGGCTAG CGGTGGGCG GGTCTTACCG CAGGCGCCAA 60
GGGCGGCCAC GGTTCACCTT CAACGAGCG GGCACCGCG GCGGACGCG GCAACGCGG 120
CAACTCCCAA GTGCTCGCG GCAACGCGCG CACGCGCGC AATGCGCGCA ACGGCGCGAG 180
CGCGGCGACG GCGGCGACCG GCGGCGCGCG CCGGACCGCG GCGTTTGGTG GCATGAGTGC 240
CAACGCGGACC AACCTGGTG AAAACGCGCG AACGCTAAC CCGGCGCGCA ACGGCGCGCG 300
CGGC 304

```

## (2) INFORMATION FOR SEQ ID NO:162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GTGGGACGCT GCGGAGGCTG TATAACAAGG ACAAATCGA CCAGCGCGCG CTGGGTGAGC  | 60   |
| TGATCGACCT ATTTAACAGT GCGCGCTTCA GCGGCGAGGG CGAGCACCGC GCGCGGATC  | 120  |
| TGATGGGTGA GGTCTACGAA TACTTCCTCG GCAATTTGCG TCGCGCGGAA GCGAAGCGGG | 180  |
| GTGGCGAGTT CTTTACCCCG CCCAGCGTGG TCAAGGTGAT CGTGGAGGTG CTGGAGCCCT | 240  |
| CGAGTGGGCG GGTGTATGAC CCGTGGTGGG GTTCCGAGG CATGTTTGTG CAGACCGAGA  | 300  |
| AGTTCACTCA CGAACACGAC GCGGATCCGA AGGATGTCTC GATCTATGGC CAGGAAGCA  | 360  |
| TTGAGGAGAC CTGGCGGATG GCGAAGATGA ACCTCGCCAT CCACGGCATC GACAACAAGG | 420  |
| GGCTCGGCGC CCGATGGAGT GATACCTTGG GCGCGGACCA GCACCCGGAC GTGCAGATGG | 480  |
| ACTAGGTGAT GCGCAATCGG CGCTTCAACA TCAAAGACTG GCGCCGCAAC GAGGAAGACC | 540  |
| CACGCTGGCG CTTGGGTGTG CCGCGCGGCA ATAAAGCCAA CTACCGATGG ATTGAGCACA | 600  |
| TCTGTACAA CTTGGCGCGG GAGGTGCGGG GCGGCGTGGT GATGGCCAAC GGTGCGATGT  | 660  |
| CGTGGAACTC CAACGGGAGG GCGGATATTC GCGCGCAAAT CGTGGAGGCG GATTGGTTT  | 720  |
| CGTGCATGGT CGCTTACCTC ACCAGGTGT TCGCGAGCAC CGGAATCCCG GTGTGCTGT   | 780  |
| GTTTTTCCG CAAAACAGG GCGCGAGGTA AGCAAGGTC TATCAACCGG TCGCGGCGG     | 840  |
| TCTGTTCAT CGAGGTGGT GAACTGGCG ACCTAGTGA CCGCGCGGAG CCGGCGCTGA     | 900  |
| CCAACGAGGA GATGTCGCG ATCGGGGATA CTTTCAGCG GAGCAGGACC ACCGCGAGC    | 960  |
| CGCGCTCGCG TGTGCTCGG GGTAAATGGG GCACTGCGCT CAACGGCGCG GCGGTGCTG   | 1020 |
| GCGCGCGCGG CGGCAACGCG GGTGTGCGG GGTGTGCTT CGGCAACGCT GTGGGCGCG    | 1080 |
| ACCGCGCGCA CGCGGCGAC GCGGCGGAG GCGGCGAGCG CAGGACGGGC GCGGCGGCG    | 1140 |
| GCAAGGCGCG CACGCGGAG AGCGTGGCG CCAGCGGCTC AGGCTTCCTC AACCTACCG    | 1200 |
| CGCGCGAGCG CGGCAACGCG GCGATGCGG GCAACGCGCG CAACGCTCTC GCGGCGGCG   | 1260 |
| GCGCGCGAGG CGTGGCGCG GCGAGCGCT GCAACGCGCG CCAGCGGCG GGTGCGAGCG    | 1320 |
| GCGCGCGGAG CGGCAAGGCG GCGAAGCGCA CCAGCGGTGC CCGGAGCGCG TCAGCGCTCA | 1380 |
| TCAAGCTCAC CGCGCGGAG GCGGCGAAG GCGGCAATGG CCGCAACGCG GCGAAGCGC    | 1440 |

(2) INFORMATION FOR SEQ ID NO:163:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single